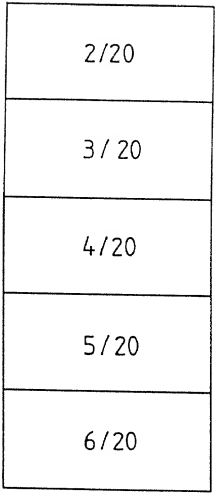


FIG 1

```
                                        CGA GTA AGT ATG GCT GTT          18
                                        Arg Val Ser Met Ala Val
                                                   -29

CAC AGA GTT AGT TTC CTT GCT CTC CTC CTC TTA TTT GGA ATG TCT CTG          66
His Arg Val Ser Phe Leu Ala Leu Leu Leu Leu Phe Gly Met Ser Leu
                        -20

CTT GTA AGC AAT GTG GAA CAT GCA GAT GCC AAG GCT TGT ACC TTA AAC          114
Leu Val Ser Asn Val Glu His Ala Asp Ala Lys Ala Cys Thr Leu Asn
-10                                  -1  1                  5

TGT GAT CCA AGA ATT GCC TAT GGA GTT TGC CCG CGT TCA GAA GAA AAG          162
Cys Asp Pro Arg Ile Ala Tyr Gly Val Cys Pro Arg Ser Glu Glu Lys
            10                  15                  20

AAG AAT GAT CGG ATA TGC ACC AAC TGT TGC GCA GGC ACG AAG GGT TGT          210
Lys Asn Asp Arg Ile Cys Thr Asn Cys Cys Ala Gly Thr Lys Gly Cys
        25                  30                  35

AAG TAC TTC AGT GAT GAT GGA ACT TTT GTT TGT GAA GGA GAG TCT GAT          258
Lys Tyr Phe Ser Asp Asp Gly Thr Phe Val Cys Glu Gly Glu Ser Asp
    40                  45                  50
```

FIG 1

```
CCT AGA AAT CCA AAG GCT TGT ACC TTA AAC TGT GAT CCA AGA ATT GCC      306
Pro Arg Asn Pro Lys Ala Cys Thr Leu Asn Cys Asp Pro Arg Ile Ala
 55                  60                  65                  70

TAT GGA GTT TGC CCG CGT TCA GAA GAA AAG AAG AAT GAT CGG ATA TGC      354
Tyr Gly Val Cys Pro Arg Ser Glu Glu Lys Lys Asn Asp Arg Ile Cys
                 75                  80                  85

ACC AAC TGT TGC GCA GGC ACG AAG GGT TGT AAG TAC TTC AGT GAT GAT      402
Thr Asn Cys Cys Ala Gly Thr Lys Gly Cys Lys Tyr Phe Ser Asp Asp
            90                  95                  100

GGA ACT TTT GTT TGT GAA GGA GAG TCT GAT CCT AGA AAT CCA AAG GCT      450
Gly Thr Phe Val Cys Glu Gly Glu Ser Asp Pro Arg Asn Pro Lys Ala
        105                 110                 115

TGT CCT CGG AAT TGC GAT CCA AGA ATT GCC TAT GGG ATT TGC CCA CTT      498
Cys Pro Arg Asn Cys Asp Pro Arg Ile Ala Tyr Gly Ile Cys Pro Leu
    120                 125                 130

GCA GAA GAA AAG AAG AAT GAT CGG ATA TGC ACC AAC TGT TGC GCA GGC      546
Ala Glu Glu Lys Lys Asn Asp Arg Ile Cys Thr Asn Cys Cys Ala Gly
135                 140                 145                 150
```

FIG 1

```
AAA AAG GGT TGT AAG TAC TTT AGT GAT GAT GGA ACT TTT GTT TGT GAA      594
Lys Lys Gly Cys Lys Tyr Phe Ser Asp Asp Gly Thr Phe Val Cys Glu
                155                 160                 165

GGA GAG TCT GAT CCT AAA AAT CCA AAG GCC TGT CCT CGG AAT TGT GAT      642
Gly Glu Ser Asp Pro Lys Asn Pro Lys Ala Cys Pro Arg Asn Cys Asp
            170                 175                 180

GGA AGA ATT GCC TAT GGG ATT TGC CCA CTT TCA GAA GAA AAG AAG AAT      690
Gly Arg Ile Ala Tyr Gly Ile Cys Pro Leu Ser Glu Glu Lys Lys Asn
        185                 190                 195

GAT CGG ATA TGC ACC AAC TGC TGC GCA GGC AAA AAG GGT TGT AAG TAC      738
Asp Arg Ile Cys Thr Asn Cys Cys Ala Gly Lys Lys Gly Cys Lys Tyr
    200                 205                 210

TTT AGT GAT GAT GGA ACT TTT GTT TGT GAA GGA GAG TCT GAT CCT AAA      786
Phe Ser Asp Asp Gly Thr Phe Val Cys Glu Gly Glu Ser Asp Pro Lys
215                 220                 225                 230

AAT CCA AAG GCT TGT CCT CGG AAT TGT GAT GGA AGA ATT GCC TAT GGG      834
Asn Pro Lys Ala Cys Pro Arg Asn Cys Asp Gly Arg Ile Ala Tyr Gly
                235                 240                 245
```

FIG 1

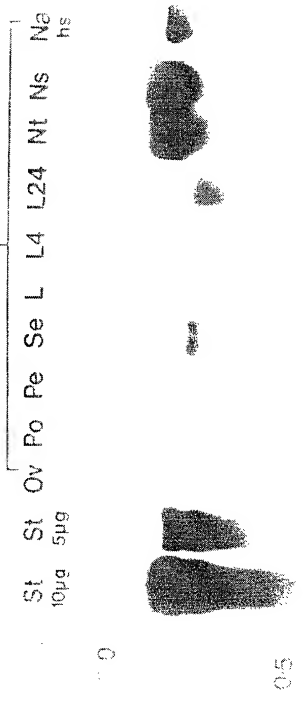
```
ATT TGC CCA CTT TCA GAA GAA AAG AAG AAT GAT CGG ATA TGC ACA AAC      882
Ile Cys Pro Leu Ser Glu Glu Lys Lys Asn Asp Arg Ile Cys Thr Asn
            250                 255                 260

TGT TGC GCA GGC AAA AAG GGC TGT AAG TAC TTT AGT GAT GAT GGA ACT      930
Cys Cys Ala Gly Lys Lys Gly Cys Lys Tyr Phe Ser Asp Asp Gly Thr
        265                 270                 275

TTT GTT TGT GAA GGA GAG TCT GAT CCT AGA AAT CCA AAG GCC TGT CCT      978
Phe Val Cys Glu Gly Glu Ser Asp Pro Arg Asn Pro Lys Ala Cys Pro
    280                 285                 290

CGG AAT TGT GAT GGA AGA ATT GCC TAT GGA ATT TGC CCA CTT TCA GAA     1026
Arg Asn Cys Asp Gly Arg Ile Ala Tyr Gly Ile Cys Pro Leu Ser Glu
295                 300                 305                 310

GAA AAG AAG AAT GAT CGG ATA TGC ACC AAT TGT TGC GCA GGC AAG AAG     1074
Glu Lys Lys Asn Asp Arg Ile Cys Thr Asn Cys Cys Ala Gly Lys Lys
                315                 320                 325

GGC TGT AAG TAC TTT AGT GAT GAT GGA ACT TTT ATT TGT GAA GGA GAA     1122
Gly Cys Lys Tyr Phe Ser Asp Asp Gly Thr Phe Ile Cys Glu Gly Glu
            330                 335                 340
```

FIG 1

```
TCT GAA TAT GCC AGC AAA GTG GAT GAA TAT GTT GGT GAA GTG GAG AAT      1170
Ser Glu Tyr Ala Ser Lys Val Asp Glu Tyr Val Gly Glu Val Glu Asn
       345                 350                 355

GAT CTC CAG AAG TCT AAG GTT GCT GTT TCC TAAGTCCTAA CTAATAATAT      1220
Asp Leu Gln Lys Ser Lys Val Ala Val Ser
    360                 365

GTAGTCTATG TATGAAACAA AGGCATGCCA ATATGCTCTG TCTTGCCTGT AATCTGTAAT  1280

ATGGTAGTGG AGCTTTTCCA CTGCCTGTTT AATAAGAAAT GGAGCACTAG TTTGTTTTAG  1340

TTAAAAAAAA AAAAAAAAAA                                           1360
```

FIG 1

FIG 2



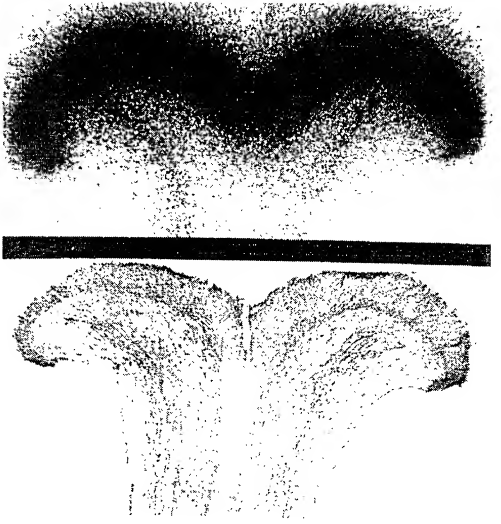


FIG 3

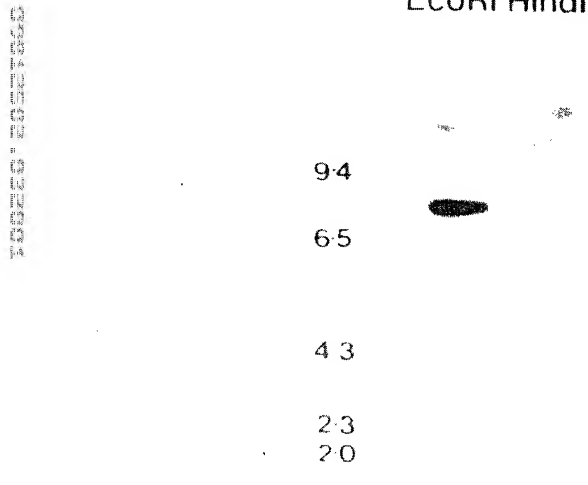


FIG 4

FIGURE 5A

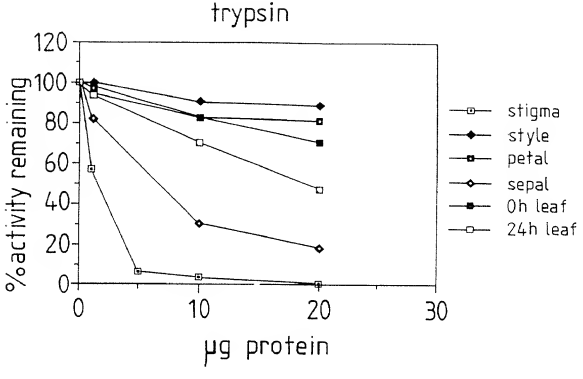
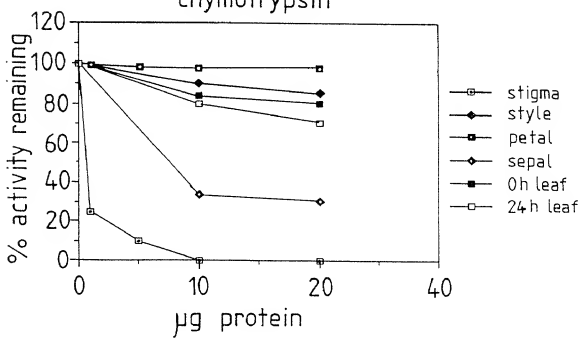


FIGURE 5B



11/20

FIG 6

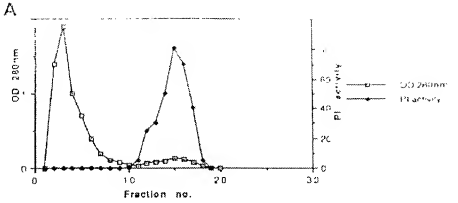
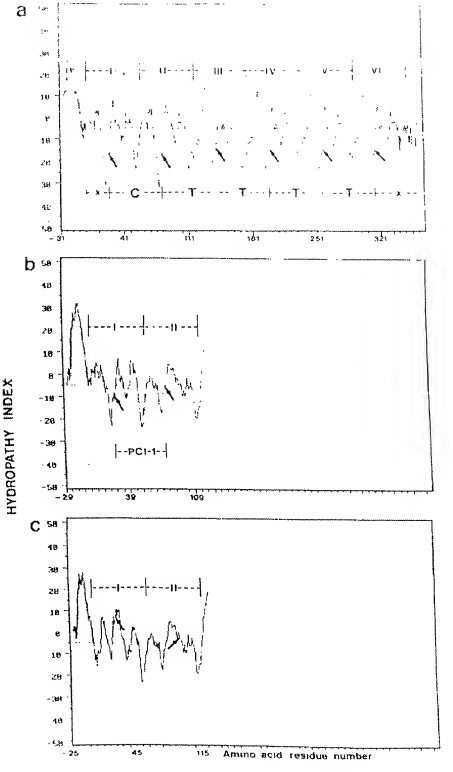

A
OD 280 nm
0
10
20
30
Fraction no.
B
-16·9
-14·4
-8·2
-6·2
-2·5
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20
C
1
2
3
-16·9
-14·4
-8·2
-6·2
-2·5

FIG 7



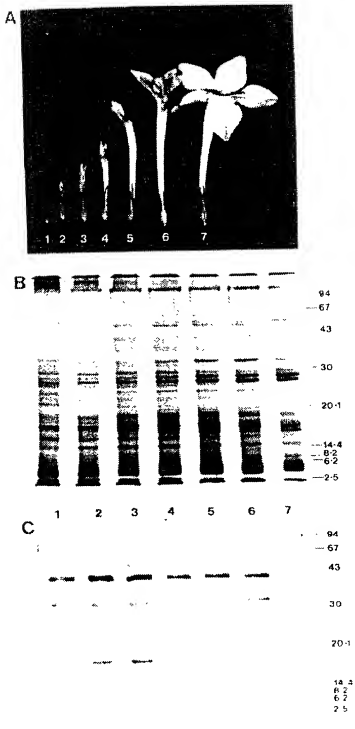
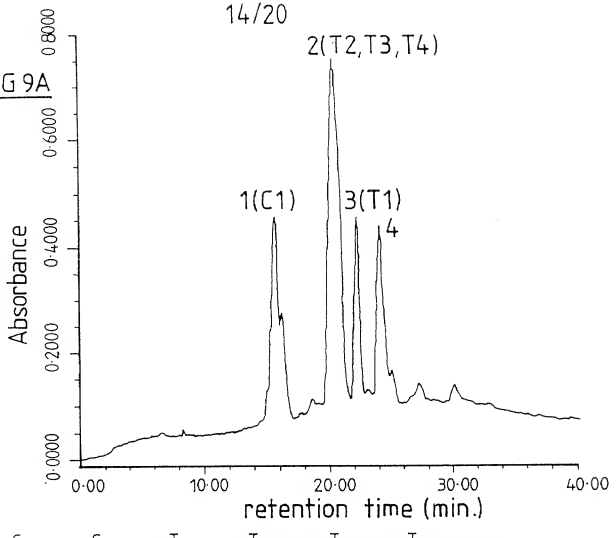

A
1 2 3 4 5 6 7
B
94
67
43
30
20·1
14·4
6·2
6·2
2·5
1 2 3 4 5 6 7
C
94
67
43
30
20·1
14·3
6·2
6·2
2·5

FIG 8

FIG 9A



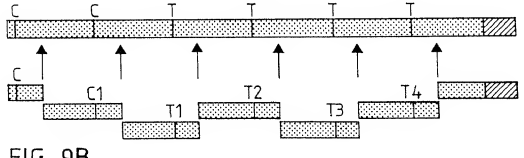


FIG 9B

```
C1 DRICTNCCAGTKGCKYFSDDGTFVCEGESDPRNPKACTLNCDPRIAYGVCPRS
T1 DRICTNCCAGTKGCKYFSDDGTFVCEGESDPRNPKACPRNCDPRIAYGICPL
T2 DRICTNCCAGKKGCKYFSDDGTFVCEGESDPKNPKACPRNCDGRIAYGICPLS
T3 DRICTNCCAGKKGCKYFSDDGTFVCEGESDPKNPKACPRNCDGRIAYGICPLS
T4 DRICTNCCAGKKGCKYFSDDGTFVCEGESDPRNPKACPRNCDGRIAYGICPLS
   1        10        20        30        40        50
```

FIGURE 9C

-10 1 10

ICP(R or L)(S or A)EEKKNDRICTNCCAG(T or K)KG

FIGURE 10

FIG 11A

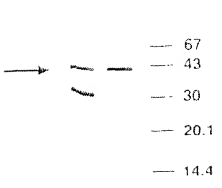
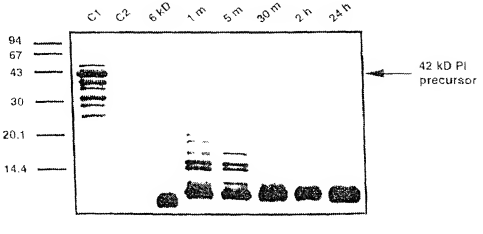


FIG 11B



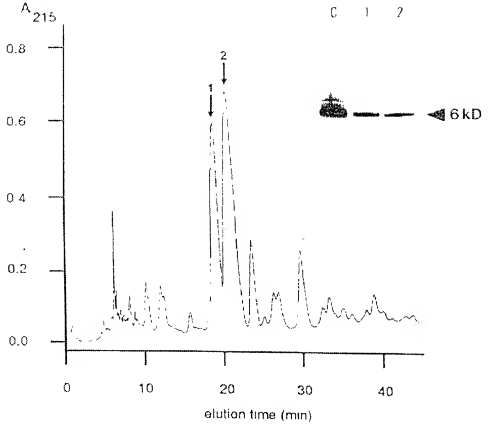


FIG 12

FIGURE 13A

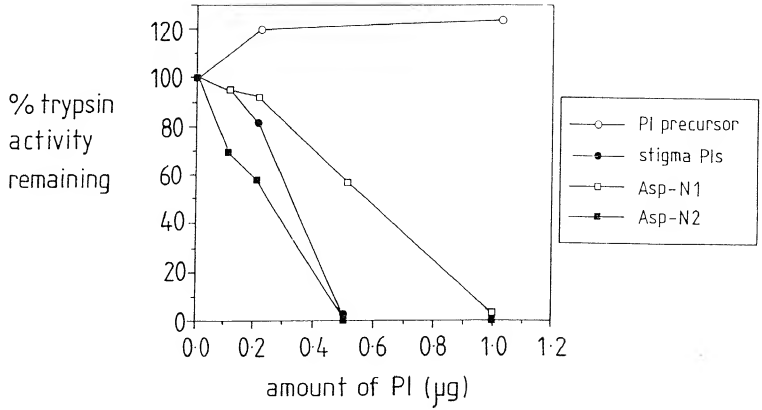
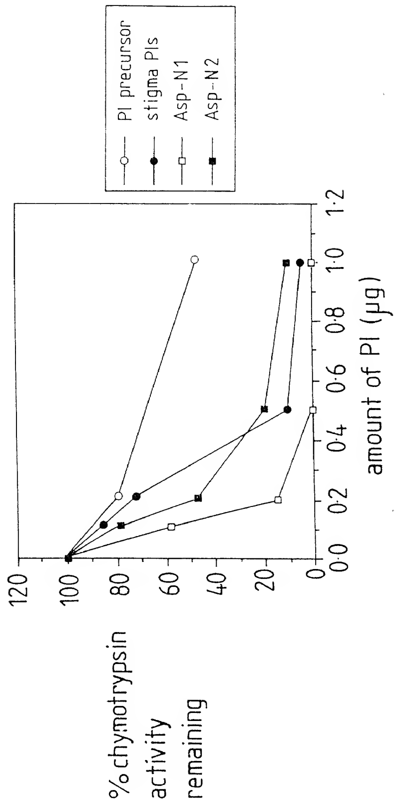

% trypsin activity remaining
120
100
80
60
40
20
0
0·0
0·2
0·4
0·6
0·8
1·0
1·2
amount of PI (µg)
PI precursor
stigma PIs
Asp-N1
Asp-N2

FIGURE 13B


PI precursor
stigma PIs
Asp-N1
Asp-N2
% chymotrypsin activity remaining
120
100
80
60
40
20
0
0·0
0·2
0·4
0·6
0·8
1·0
1·2
amount of PI (µg)

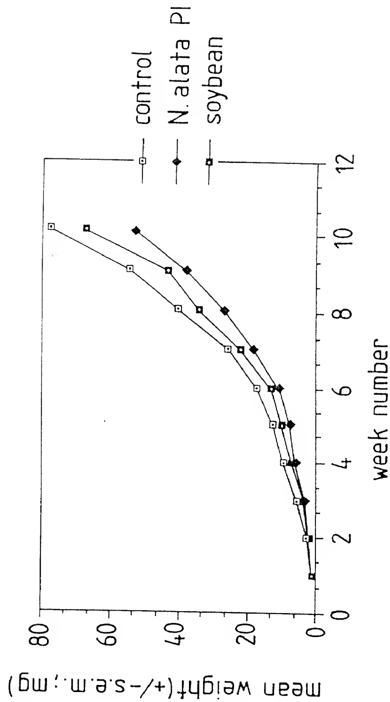

mean weight(+/-s.e.m.; mg)
0
20
40
60
80
0
2
4
6
8
10
12
week number
control
N. alata PI
soybean

FIGURE 14